

APR 24 1998

PATENT

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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : Lorin R. DeBonte et al.
Serial No.: 08/572,027
Filed : December, 14, 1995
Title : PLANTS HAVING MUTANT SEQUENCES THAT CONFER ALTERED
FATTY ACID PROFILES

Art Unit: 1649
Examiner: G. Benzion

Assistant Commissioner for Patents
Washington, DC 20231

DECLARATION UNDER 37 CFR §1.132 OF GUO-HUA MIAO

I, Guo-Hua Miao, declare as follows:

1. That I am a citizen of the People's Republic of China and presently live at 202 Cherry Blossom Place, Hockessin, Delaware.

2. That I received a Bachelor of Science degree in Biology from Shanghai Normal University, Shanghai, China in 1982, a Master of Science degree in Plant Physiology from Shanghai Institute of Plant Physiology, Chinese Academy of Science, Shanghai, China in 1984 and a Doctor of Philosophy degree in Molecular, Cellular and Developmental Biology from Ohio State University, Columbus, Ohio in 1991.

3. That I was employed as a research associate at the Biotechnology Center, Ohio State University, Columbus, Ohio from 1991 to 1993.

4. That I am presently employed as a Senior Research Molecular Biologist by DuPont Agricultural Products, a division of E. I. Dupont de Nemours, Inc. and have been so employed since 1993.

5. That, as an employee of DuPont, I determined Fad2 desaturase coding sequences obtained from canola lines Westar and Q508. Westar is a canola variety having no known mutations in

Declaration of Guo-Hau Miao
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Fad2 desaturase genes. Q508 is a line derived from Westar by mutagenesis. A copy of four microfilmed pages from my laboratory notebook is attached as Exhibit A (Notebook F79066, pages 140-143). These notebook pages show the DNA sequences and deduced amino acid sequences that were obtained by me or under my supervision. The dates on these four pages, all of which are prior to December 14, 1995, have been blocked out.

The DNA and deduced amino acid sequence of Fad2-F from line Q508 is shown at pages 140-141. The Q508 Fad2-F sequence contains a mutation at nucleotide 515 compared to the wild-type Westar sequence, as indicated at page 140 of the notebook. The wild-type nucleotide at this position is T, and the mutant nucleotide is A. Based on the information at pages 140-141, the mutant Q508 Fad2-F and wild-type Fad2-F sequences contain a G at position 316.

The DNA and deduced amino acid sequences of Fad2-D from the Westar variety is shown at pages 142-143. The wild-type Fad2-D sequence contains a G at nucleotide 316, whereas the IMC 129 mutant Fad2-D sequence contains an A, as indicated at page 142 of the notebook. Based on the information at pages 142-143, the wild-type Fad2-D and mutant IMC 129 Fad2-D sequences contain a T at position 515.

6. After these sequences were determined, the mutant Fad2-D sequence and the mutant Fad2-F sequence were mailed to Ronald Lundquist. A copy of the sequences that were mailed, as well as the cover letter, are attached hereto as Exhibit B. The dates on these pages, all of which are prior to December 14, 1995, have been blocked out. A comparison of the nucleotide sequences in my laboratory notebook to those enclosed with the letter to Ronald Lundquist indicates that the sequences enclosed in the letter were incorrectly labeled. The sequence labeled as "f-gene, 508" corresponds to the wild-type Fad2-D sequence of my

Declaration of Guo-Hau Miao
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notebook, with the Q508 mutation inserted at position 515. The sequence labeled as "d-gene, 129" corresponds to the wild-type Fad2-F sequence of my notebook, with the IMC 129 mutation inserted at position 316. It appears that the sequence labels were inadvertently switched and the D and F mutations added to the sequence prior to mailing the information to Mr. Lundquist.

7. I further declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the instant patent application or any patent issuing thereon.

Dated: 10/1/95


Guo-Hua Miao, Ph.D.

14066.M11

E. I. DUPONT DE NEMOURS AND COMPANY

140

E 79066

Page No. TITLE

Book No. PURPOSE

cont'd from Page 187

DATE

cont'd from Page 187

5	10	15	20	25	30	35	40	45
ATG	CCT	CCA	GTT	GGG	AGA	ATG	CAA	GTC
TCT	CCT	CCC	TCC	TCT	ATC	ATG	AGG	TCT
TAC	CCA	CGT	CCA	CCT	TCT	TAC	GTT	CCA
M	G	A	G	G	R	M	Q	V
50	55	60	65	70	75	80	85	90
GAA	ACC	GAC	ACC	ATC	AAG	CGG	CTA	CCC
CTT	TGG	CTG	TGG	TAC	TTC	GGG	CAT	TCC
E	T	D	T	I	X	R	V	P
100	105	110	115	120	125	130	135	140
GTC	CCA	GAA	CTC	AAG	AAA	CCA	ATC	CCA
CAG	CCT	CCT	GAT	GAG	TTC	TTC	TGG	GGG
V	G	E	L	K	R	A	I	P
145	150	155	160	165	170	175	180	185
ATG	CCT	CGC	TCT	TTC	TGG	GAC	ATC	ATC
TAG	GGG	GGG	AGA	AGG	ATG	GAC	TAC	GGG
I	P	R	S	F	S	T	L	I
195	200	205	210	215	220	225	230	235
TGC	TTC	TAC	TAC	NTG	GGC	ACC	ACT	TAC
AGG	AGG	ATG	ATG	AGG	TGG	TGA	ATG	AAG
C	F	Y	X	A	T	T	Y	F
245	250	255	260	265	270	275	280	285
CTC	TCC	TAC	TTC	GGC	TGG	CCT	TTC	TAC
CAG	AGG	ATG	AAG	CGG	ACC	GGG	AGG	GGG
L	S	Y	F	A	W	P	L	T
290	295	300	305	310	315	320	325	330
CTA	ACC	GGC	GTC	TGG	GGC	ATA	GGC	GGC
CAT	TGG	CCG	CAG	ACC	CAG	TAT	GGG	TGC
340	345	350	355	360	365	370	375	380
ACC	GAC	TAC	CGG	TGG	CCT	GAC	ACC	GTC
TGG	CTG	ATG	ATG	AGG	ATC	TTC	GGT	TGC
I	D	Y	Q	W	L	D	D	T
385	390	395	400	405	410	415	420	425
TTC	CTC	CTC	GGC	CCT	TAC	TTC	TGG	AGG
AGG	GAG	GAG	GGG	AGG	ATG	AGG	GGG	TTC
F	L	V	P	Y	F	S	W	K
435	440	445	450	455	460	465	470	475
CAT	TCC	AAC	ACT	GGC	TGC	CTC	GGG	TTC
ATA	AGG	ITG	TGA	CCG	AGG	AGG	TCT	TCT
H	S	T	S	S	L	E	R	D
485	490	495	500	505	510	515	520	525
AAG	AAG	TCA	GAC	ATC	AAG	TGG	TAC	GGG
TTC	TTC	ACT	CTG	AGT	TTC	ACC	ATG	CGG
I	K	S	D	I	K	Y	S	T
530	535	540	545	550	555	560	565	570
GGA	CGC	ACC	GTG	ATC	TTA	ACG	GTT	ACT
CTT	GGG	TGG	ATG	TTA	ACG	GTT	ACG	TTC
G	R	T	V	M	L	T	V	T
580	585	590	595	600	605	610	615	620
TAC	TTA	GGC	TTC	ATC	TGG	CCA	AGA	CCT
ATG	ATG	ATG	ATG	CGG	AGG	ATG	TCT	TCT
T	L	A	F	V	S	G	T	D

EXPERIMENTER

John Miller

DATE

WITNESSED BY

C.H.

DATE

DNA and deduced

protein sequence

of *caeca* F002

(p) from 0508.

CTC was present

in water and

12.9 always.

Thus in 0508

a Histidine was

replaces leucine

position 514-516 bp

This mutation

P in D clone

is specific to

(leucine)

0508

Sequence in this

region was

confirmed from

both strands

TITLE

cont'd

DATE

Page No.

141

PURPOSE

cont'd

Book No.

79066

625 630 635 640 645 650 655 660 665 670
 TCC CAT TTC CAC CCC AAC GCT CCC ATC TAC AAC GAC CCC GAG CGT CTC
 ACG GTA AAG GTG GGG TTG CGA CGG TAG ATG TTG CTG CGG CTC GCA GAG
 C H F H P N A P I Y N D R E R L
 675 680 685 690 695 700 705 710 715 720
 CAG ATA TAC ATC TCC GAC GCT GGC ATC CTC GGC GTC TGC TAC GCT CTC
 GTC TAT ATG TAG AGG CTG CGA CGG TAG GAG CGG CAG AGG ATG CCA GAG
 Q I Y Z S D A G I L A V C Y G L
 725 730 735 740 745 750 755 760 765
 TTC CGT TAC GCC GGC GGC CAG GGA GTG GGC TCC ATG GTC TCC TCC TAC
 AAG GCA ATG CGG CGG CGG GTC CCT CAC CGG AGC TAC CAC AGC AAG ATG
 F R Y A A G Q G V A S N V C F Y
 770 775 780 785 790 795 800 805 810 815
 GGA GTC CGG CTT CTG ATT GTC ATT GGT TTC CTC GTG TGC ATC ACT TAC
 CCT CAG GGC GAA GAC TAA CAG TTA CCA AAG GAG CAC AAC TAG TGA ATG
 G V P L L I V N G F L V L I T Y
 820 825 830 835 840 845 850 855 860
 TTG CAG CAC ACC CAT CCT TCC CTG CCT CAC TAC GAT TCG TCC GAG TGG
 AAC GTC GTG TGC GAA AGG GAC GGA GTG ATG CTA AGC AGG CCT ACC
 L Q H T H P S L P H Y D S S E W
 865 870 875 880 885 890 895 900 905 910
 GAT TGG TTC AGG GGA GCT TTG GCT ACC GTC GAC AGA GAC TAC GGA ATC
 CTA ACC AAG TCC CCT CGA AAC CGA TGG CAA CCT TCT CTG ATG CCT TAG
 D W F R G A L A T V D R D Y G Y
 915 920 925 930 935 940 945 950 955 960
 TTG AAC AAG GTC TTC CAC ATT ATT ACC GAC AAG GAC GTG GCC CAT CAT
 AAC TTG TTC CAG AAC GTG TTA TAA TGG CTG TGC GTG CAC CGG GTC GTC
 L N K V F H N I T D T H V A H H
 965 970 975 980 985 990 995 1000 1005
 CCG TTC TCC ACG ATG CGG CAT TAT CAC GGU ATG GAA GCT ACC AAG GCG
 GGC AAC AGG TGC TAC CGC GTC ATA GTC CGG TAC CCT CCA TGG TTG CCC
 P F S T M P H Y H A M E A T R A
 1010 1015 1020 1025 1030 1035 1040 1045 1050 1055
 ATA AAG CGG ATA CTG GGA CAC TAT TAT CAC TTC GAT GGG AGC CGG GTG
 ATT TTC GGC TAT GAC CCT CTC ATA ATA GTC AAC CTA CCC TGC GGC CAC
 I K P I L G E Y Y Q F D G T P V
 1060 1065 1070 1075 1080 1085 1090 1095 1100
 GTT AAG CGG ATG TGG AGG GAG GCG AAC GAG TGT ATC DAT GTG GAA CGG
 CAA TTC CGC TAC ACC TCC CTC CGG TTC CTC ACA TAG ATA CGC CCT GGC
 V K A M W R E A K E C I Y V E
 1105 1110 1115 1120 1125 1130 1135 1140 1145 1150
 GAC AGG CAA GGT GAG AAC AAA GGT GTG TTC TGG TAC AAC ATT AAC TTA
 CGG TCC GTT CCA CTC TTC TTT CCA CAC AAC AGC ATG TGC TTA TCC ATT
 D R Q G E K K G V F W Y N N K L
 1155 1160 1165 1170 1175 1180 1185
 TGA GCA ATT GAT GAT GGT GAA AGA ATT CAC TAG
 ACT CCT ATA CTA CTA CCA CCT TCT TTA GTG ATC
 * G Y D D G E R N H *

See prime location

on page 134

In Q508

a Mai S.L.

was last seen

on the sequence

analysis.

CTTC (cont'd)

CCAC (cont'd)

Mai + T (CTTC)

Therefore, Mai

will provide a

single way to

distinguish Q508

and AT + T.

EXPERIMENTER

Seth D.

DATE

WITNESSED BY

CH

DATE

E. I. DUPONT DE NEMOURS AND COMPANY

142

Page No. 1TITLE conf'dDATE 10/10/68

E 79066

Book No. 1PURPOSE conf'd

1000 900 800 700 600 500 400 300 200 100

ATG GGT GCA GGT GGA AGA ATG CAA GTG TCT CCT CCC TCC AAA AAC TCT
 TAC GCA GGT CCA CCT TCT TAC GTT CAC AGA GGA GGG AGG TTT TTC AGA
 M G A G G R M Q V S P P S K K S >
 50 55 60 65 70 75 80 85 90 95
 GAA ACC GAC AAC ATC AAC CGC GAA CCC TCC GAG AGA CGG CCC TTC ACT
 CCT TCG CTG TTG TAG TCC GGG CAT GGG AGG CTC TGT GGC GGG AGG TGA
 E T D N I K V P C E T P P P T >
 100 105 110 115 120 125 130 135 140
 GTC GGA GAA CTC AAC AAA GCA ATC CCA CGG CAC TGT TTC AAA CGG TCG
 CAG CCT CTT GAG TTC TTT CGT TAG GGT GGG GTC AGA AGG TTT CGG AGG
 V G E L K K A I P P H C F K R S >
 145 150 155 160 165 170 175 180 185 190
 ATC CCT CGC TCT TTC TCC CTC ATC TGG GAC ATC ATC AIA GCC TCC
 TAG GGA GGG AGA AGG AGG ATG GAG TAG ACC CTG TAG TAG TAT CGG AGG
 I P R S E S Y L I W D I I I A S >
 195 200 205 210 215 220 225 230 235 240
 *TGC TTC TAC TAC GTC GGC ACC ACT TAC TTC CCT CTC CCT CGC CCT
 ACG AGG ATG ATG CAG CGG TGG TGA ATG AGG GGA GAG GAG GGA GTC GGA
 C F Y Y V A T T Y F P L L P H P >
 245 250 255 260 265 270 275 280 285
 CTC TCC TAC TTC GGC TCC CCT CTC TAC TGG GGC TGC CAG GGC TCC GTC
 GAG AGG ACC GGA GAG ATG ACC CGG AGG GTC CGG AGG CAG CAG
 L S Y F A W P L Y W A C >
 290 295 300 305 310 315 320 325 330 335
 A (2K) → 129, 425
 CTA ACC GGC GTC TGG GTC ATA GGC CAC GAG TCC GGC CAC CAC GGC TTC
 GAT TGG CCG CAG ACC CAG TAT CCT GTG CTC ACG CGG GTG GTG GGG AGG
 I T C G Y H V E R D E V F V P L L P H P >
 340 345 350 355 360 365 370 375 380
 AGC GAC TAC CAC TGG CTC GAC GAC ACC GTC GGC CTC ATC ATC TAC CCT
 TCG CTG ATG CTC ACC CAC CTC TGG CAG CGG CAG TAG AGC GTG AGG
 D T V G L I F H I S >
 385 390 395 400 405 410 415 420 425 430
 TTC CTC CTC GTC CCT TAC TTC TCC TGG AGG TAC AGT CAT CGA CGC CAC
 AAG GAG GAG CAC CGA ATG AGG AGG ACC TTC ATG TCA GTA CCT GCG GTG
 F L L V P Y F S W K Y S H R R H >
 435 440 445 450 455 460 465 470 475 480
 CAT TCC AAC ACT GGC TCC CTC GAG AGA GAC GAA GTG TTT GTC CCC AGG
 GTA AGG TTG TGA CGG AGG GAG CTC TCT CTG CCT CAC AAA CAG GGG TTC
 H S N T G S L E R D E V F V P R >
 485 490 495 500 505 510 515 520 525
 AAC RAG TCA GAC ATC AAG TGG TAC CGC AGG TAC CTC AAC AAC CCT TTG
 TTC ATG CCT TAG TTC ACC ATC CGG TTC ATG GAG TTS TCG GGA AAC
 K R S D I K W Y G K Y L N N P L >
 530 535 540 545 550 555 560 565 570 575
 CGA CGC ACC GTG ATG TTA AGC CCT CGA CCT ACT CTC GGC TGG CCT TTG
 CCT CGG TGC CAC TAC AAA TGC CAA GTC AGA GAG CGG ACC GCA AAC
 G R T V M L T V Q F T L G W P L >
 580 585 590 595 600 605 610 615 620
 TAC TTA GGC TTC AAC GTC TGG GGG AGA CCT TAC GAC GGC GGG TTG OCT
 ATG ATT CGG AGG TTG CAG AGC CCC TCT GCA ATG CTC CGG CGG AGG CGA
 Y L A F B V S G R P Y D G C F A >

DNA and deduced
 protein sequence
 from vector FAD2

(B) clone

In 129 and

Q508 clones

(E)

CGS was converted
to AAC<-(k)

Flag mutation

was found in

Flag clone only

BD bat occur

in both 129 and

Q508 mutant

Lines

Again, flag

region was

confirmed from

EXPERIMENTER

John D. Williams

DATE

WITNESSED BY

Elmer Aggen

DATE

E. I. DUPONT DE NEMOURS AND COMPANY

TITLE conf'd DATE _____ Page No. 143
 PURPOSE conf'd Book No. E 79066

625 630 635 640 645 650 655 660 665 670
 TCC CAT TTC CGC CGC AAC GCT CCC ATC TAC AAC GAC GAC CGC GAG CGT CTC
 ACG GTC AAG GTG CGG TTG CGA GGG TAG ATG TTG CTG GCG CTC GCA GAG
 C H E H P N A P I Y N D R E R L>
 675 680 685 690 695 700 705 710 715 720
 CGG ATG TAC ATC TCC GAC GCT GGC ATC CTC GTC TCC TAC GCT CTC
 GTC TAT ATG TAC AGG CTG CGA CGG TAG CGC CGG CGG AGG ATG CGA GAG
 Q I Y I S D A C I L A V C T G L>
 725 730 735 740 745 750 755 760 765
 TAC CGC TAC GCT GGT GTC CAA CGA GTT GGC TCC ATG GTC TCC TTC TAC
 ATG GGG ATG CGA CGA CAG GTT CCT CAA CGG ACC TAC CAG ACC AAG ATG
 Y R T A A V Q G V A S M V C F Y>
 770 775 780 785 790 795 800 805 810 815
 GGA GTT CCG CCT CTG ATT GTC AAT GGG TTG TTA GTT TTG ATG ACT TAC
 CCT CAA CGC GAA GAC TAA CGG TAA CGG AAG AAT CAA AAC TAG TGA ATG
 G U P L L I V N G F L V L I T Y>
 820 825 830 835 840 845 850 855 860
 TIG CAG CAC ACG CAT CCT TCC CTG CCT CAC TAT GAC TCC TCT GAG TGG
 AAC GTC GTG TGC GTC GAA CGG GAC CGA GTG ATA CTG AGC AGA CTC ACC
 L Q H T H P S L P H Y D S S E W>
 865 870 875 880 885 890 895 900 905 910
 GAT TGG TTG AGG CGG GCA GCT TTG CGC ACC GTT GAC AGA GAC TAC CGA ATC
 CTA ACC AAC TCC CCT CGA AAC CGG CGC CGC ATA CTG CCT ATG CCT TAC
 D W L R G A L A T V D R D Y G>
 915 920 925 930 935 940 945 950 955 960
 TTG AAC AAG GTC TIC CAG AAT ATC ACC GAC AGC CAC GTC CGG CAT CAC
 AAC TTC TTC CAG AAG GTG TTA TAG TCC CTG TCC GTG CAC CGC GTC CGC
 L N K V F H N I T D T H V A H H>
 965 970 975 980 985 990 995 1000 1005
 CTG TTC TCG ACC ATG CGG CAT TAT CAT CGG ATG GAA GCT ACC AAC CGG
 GAC AAG AGC TGG TAC CGC GTC ATA GTC CGC TAC CCT CGA TCC TTC CGC
 L F S T M P H Y H A M R A T K A>
 1010 1015 1020 1025 1030 1035 1040 1045 1050 1055
 ATA AAG CGG ATA CTG CGA GAG TAT TAT CAG TTG CAT CGG AGG CGG CGG STG
 TAT TTG CGC TAT GAC CCT CTC ATA ATA GTC AAC GTC CCC TCC CGC CAC
 I K P I L G E Y Y Q L H G T P V>
 1060 1065 1070 1075 1080 1085 1090 1095 1100
 GTT AAC CGG ATG TGC AGG GAG CGG AAC GAG TGT ATC TAT GTG GAA CGG
 CAA TIC CGC TAT AGC TCC GTC CCT CGC TIC CTC ACA TAG ATA CGC CCT CGC
 V K A M W R E A K E C I Y V E P>
 1105 1110 1115 1120 1125 1130 1135 1140 1145 1150
 GAC AGG CGA GGT GAG AAA GGT CGC TTG TGG TAC AAC AAT AAC TTA
 CTG TCC GTT CGA CTC TTC TTT CGA CGC AAC AGC ATG TGG TTA TTC ATG
 D R Q G E K K G V F W Y N N X>
 1155 1160 1165 1170
 TCA AGC AAA GAA GAA AGC AT
 ACT TCC TTT CCT CCT TGT TA
 S K E E T D>

With steady

(see page 134)

from prime location.

Total 5 segments

129 and 954

clones (each unit

one) were

Sequence by

prime DR

(see page 134)

and showed the
same mutation.

Thus it appears

to be true

mutation.

This will be
further confirmed
by re RT-PCR
and from 129 - 954
and sequenced by
DR prime

EXPERIMENTER

George P. L.

DATE

WITNESSED BY

C. Dugay

DATE



RECEIVED

AGRICULTURAL PRODUCTS
Experimental Station
P.O. Box 80402
Wilmington, Delaware 19880-0402

RONALD C. LUNDQUIST

Mr. Ronald Lundquist
Fisher Richardson
330 Dain Bosworth Tower
60 S. 6th St.
Minneapolis, Minnesota 55402

Dear Ron:

It was very nice speaking with you over the phone on Monday. I am sending you the information about the molecular analysis of IMC129 and IMCQ508 mutations, which you requested for IMC129 and IMCQ508 patent application. A disc containing the nucleotide sequences for both canola FAD2 genes (D and F) are also included.

As we discussed over the phone, IMCQ508 mutation was identified based on sequencing of cDNA clones isolated from IMCQ508 mutant, however, the mutation had not been confirmed as we did for IMC129 mutation. Therefore, we might need to further confirm the mutation, if we would like to include IMCQ508 in the patent application. Please feel free to contact me if I can provide you any additional information about the two mutants.

Sincerely,

Guo-Hua Miao, Ph.D.
Research Molecular Biologist

CC: W. R. Majarian

Encl.

8:53 AM

5	10	15	20	25	30	35	40	45	50
*	*	*	*	*	*	*	*	*	*
ATGGGTGCAG GTGGAAGAAT GCAAGTGTCT CCTCCCTCCA AAAAGTCTGA									
TACCCACGTC CACCTTCITA CGTTCACAGA GGAGGGAGGT TTTTCAGACT									
55	60	65	70	75	80	85	90	95	100
*	*	*	*	*	*	*	*	*	*
AACCAGACAAC ATCAAGCGCG TACCCCTGCAG GACACCGCCC TTCACTGTGC									
TTGGCTGTTG TAGTTCGCGC ATGGGACGCT CTGTGGCGGG AAGTGACAGC									
105	110	115	120	125	130	135	140	145	150
*	*	*	*	*	*	*	*	*	*
GAGAACTCAA GAAAGCAATC CCACCCGCACT GTTTCAAACG CTCGATCCCT									
CTCTTGAGTT CTTTCGTTAG GGTGGCGTGA CAAAGTTGC GAGCTAGGGA									
155	160	165	170	175	180	185	190	195	200
*	*	*	*	*	*	*	*	*	*
CGCTCTTCT CCTACCTCAT CTGGGACATC ATCATAGCCT CCTGCTTCTA									
GCGAGAAAGA GGATGGAGTA GACCCTGTAG TAGTATCGGA GGACGAAGAT									
205	210	215	220	225	230	235	240	245	250
*	*	*	*	*	*	*	*	*	*
CTACGTCGCC ACCACTTACT TCCCTCTCCT CCCTCACCCCT CTCTCCTACT									
GATGCAGCGG TGGTGAATGA AGGGAGAGGA GGGAGTGGGA GAGAGGATGA									
255	260	265	270	275	280	285	290	295	300
*	*	*	*	*	*	*	*	*	*
TCGCCTGGCC TCTCTACTGG GCCTGCCAGG GCTGCGTCCT AACCGGCGTC									
AGCGGACCGG AGAGATGACC CGGACGGTCC CGACGCAGGA TTGGCCGCAG									
305	310	315	320	325	330	335	340	345	350
*	*	*	*	*	*	*	*	*	*
TGGGTCACTAG CCCACAGTG CGGCCACAC GCCTTCAGCG ACTACCAGTG									
ACCCAGTATC GGGTGTCAC GCCGGTGGTG CGGAAGTCGC TGATGGTCAC									
355	360	365	370	375	380	385	390	395	400
*	*	*	*	*	*	*	*	*	*
GCTGGACGAC ACCGTCGGCC TCATCTTCCA CTCTTCTCCT CTCGTCCCTT									
CGACCTGCTG TGGCAGCCGG AGTAAAGGT GAGGAAGGAG GAGCAGGGAA									
405	410	415	420	425	430	435	440	445	450
*	*	*	*	*	*	*	*	*	*
ACTTCTCCTG GAAGTACAGT CATCGACGCC ACCATTCAA CACTGGCTCC									
TGAAGAGGAC CTTCATGTCA GTAGCTGCGG TGGTAAGGTT GTGACCGAGG									
455	460	465	470	475	480	485	490	495	500
*	*	*	*	*	*	*	*	*	*
CTCGAGAGAG ACGAAGTGTG TGTCCCCAAG AAGAAAGTCAG ACATCAAGTG									
GAGCTCTCTC TGCTTCACAA ACAGGGGTTTC TTCTTCAGTC TGTAGTTCAC									
505	510	515	520	525	530	535	540	545	550
*	*	*	*	*	*	*	*	*	*
GTACGGCAAG TACCAACAA ACCCTTTGGG ACGCACCGTG ATGTTAACGG									
CATGCCGTTTC ATGGAGTTGT TGGGAAACCC TGCGTGGCAC TACAATTGCC									
555	560	565	570	575	580	585	590	595	600
*	*	*	*	*	*	*	*	*	*
TTCAGTTCAC TCTCGGCTGG CCTTTGTACT TAGCCTTCAA CGTCTCGGGG									
AAGTCAAGTG AGAGCCGACC GGAAACATGA ATCGGAAGTT GCAGAGCCCC									
605	610	615	620	625	630	635	640	645	650
*	*	*	*	*	*	*	*	*	*
AGACCTTACG ACGGCGGCTT CGCTTGCCAT TTCCACCCCA ACGCTCCCCAT									

8:53 AM

TCTGGAATGC TGCCGCCGAA GCGAACGGTA AAGGTGGGGT TGCGAGGGTA

655	660	665	670	675	680	685	690	695	700
*	*	*	*	*	*	*	*	*	*
CTACAAACGAC	CGCGAGCGTC	TCCAGATATA	CATCTCCGAC	GCTGGCATCC					
GATGTTGCTG	GCGCTCGCAG	AGGTCTATAT	GTAGAGGCTG	CGACCGTAGG					
705	710	715	720	725	730	735	740	745	750
*	*	*	*	*	*	*	*	*	*
TCGCCGCTCTG	CTACGGTCTC	TACCGCTACG	CTGCTGTCCA	AGGAGTTGCC					
AGCGGCAGAC	GATGCCAGAG	ATGGCGATGC	GACGACAGGT	TCCTCAACGG					
755	760	765	770	775	780	785	790	795	800
*	*	*	*	*	*	*	*	*	*
TCGATGGTCT	GCTTCTACGG	AGTTCCGCTT	CTGATTGTCA	ATGGGTTCTT					
AGCTACCAGA	CGAAGATGCC	TCAAGGCGAA	GACTAACAGT	TACCCAAGAA					
805	810	815	820	825	830	835	840	845	850
*	*	*	*	*	*	*	*	*	*
AGTTTGATC	ACTTACTTGC	AGCACACGCA	TCCTTCCCTG	CCTCACTATG					
TCAAAACTAG	TGAATGAAGC	TCGTGTGCGT	AGGAAGGGAC	GGAGTGATAC					
855	860	865	870	875	880	885	890	895	900
*	*	*	*	*	*	*	*	*	*
ACTCGTCTGA	GTGGGATTGG	TTGAGGGAGG	CTTTGGCCAC	CGTTGACAGA					
TGAGCAGACT	CACCTTAACC	AACTCCCCTC	GAAACCGGTG	GCAACTGTCT					
905	910	915	920	925	930	935	940	945	950
*	*	*	*	*	*	*	*	*	*
GACTACGGAA	TCTTGAACAA	GGTCTTCCAC	AATATCACGG	ACACGCACGT					
CTGATGCCTT	AGAACTTGTG	CCAGAAGGTG	TTATAGTGCC	TGTGCGTGCA					
955	960	965	970	975	980	985	990	995	1000
*	*	*	*	*	*	*	*	*	*
GGCGCATCAC	CTGTTCTCGA	CCATGCCGCA	TTATCATGCG	ATGGAAGCTA					
CCGCGTAGTG	GACAAGAGCT	GGTACGGCGT	AATAGTACGC	TACCTTCGAT					
1005	1010	1015	1020	1025	1030	1035	1040	1045	1050
*	*	*	*	*	*	*	*	*	*
CGAAGGCGAT	AAAGCCGATA	CTGGGAGAGT	ATTATCAGTT	GCATGGGACG					
GCTTCCGCTA	TTTCGGCTAT	GACCCTCTCA	TAATAGTCAA	CGTACCCCTGC					
1055	1060	1065	1070	1075	1080	1085	1090	1095	1100
*	*	*	*	*	*	*	*	*	*
CCGGTGGTTA	AGGCGATGTG	GAGGGAGGCG	AAGGAGTGTG	TCTATGTGGA					
GGCCACCAAT	TCCGCTACAC	CTCCCTCCGC	TTCCCTCACAT	AGATACACCT					
1105	1110	1115	1120	1125	1130	1135	1140	1145	1150
*	*	*	*	*	*	*	*	*	*
ACCGGACAGG	CAAGGTGAGA	AGAAAGGTGT	GTTCTGGTAC	AACAATAAGT					
TGGCCTGTCC	GTTCCACTCT	TCTTCCACAA	CAAGACCATG	TTGTTATTCA					
1155	1160	1165	1170	*	*				
TATGAAGCAA	AGAAGAAACA	AT							
ATACTTCGTT	TCTTCTTTGT	TA							

Sequence Range: 1 to 1172

5	10	15	20	25	30	35	40	45							
*	*	*	*	*	*	*	*	*							
ATG	GGT	GCA	GGT	GGA	AGA	ATG	CAA	GTG	TCT	CCT	CCC	TCC	AAA	AAG	TCT
TAC	CCA	CGT	CCA	CCT	TCT	TAC	GTT	CAC	AGA	GGA	GGG	AGG	TTT	TTC	AGA
M	G	A	G	G	R	M	Q	V	S	P	P	S	K	K	S>
50	55	60	65	70	75	80	85	90	95	*	*	*	*	*	*
GAA	ACC	GAC	AAC	ATC	AAG	CGC	GTA	CCC	TGC	GAG	ACA	CCG	CCC	TTC	ACT
CTT	TGG	CTG	TTG	TAG	TTC	GCG	CAT	GGG	ACG	CTC	TGT	GGC	GGG	AAG	TGA
E	T	D	N	I	K	R	V	P	C	E	T	P	P	F	T>
100	105	110	115	120	125	130	135	140	*	*	*	*	*	*	*
GTC	GGA	GAA	CTC	AAG	AAA	GCA	ATC	CCA	CCG	CAC	TGT	TTC	AAA	CGC	TCG
CAG	CCT	CTT	GAG	TTC	TTT	CGT	TAG	GGT	GGC	GTG	ACA	AAG	TTT	GCG	AGC
V	G	E	L	K	K	A	I	P	P	H	C	F	K	R	S>
145	150	155	160	165	170	175	180	185	190	*	*	*	*	*	*
ATC	CCT	CGC	TCT	TTC	TCC	TAC	CTC	ATC	TGG	GAC	ATC	ATC	ATA	GCC	TCC
TAG	GGA	GCG	AGA	AAG	AGG	ATG	GAG	TAG	ACC	CTG	TAG	TAG	TAT	CGG	AGG
I	P	R	S	F	S	Y	L	I	W	D	I	I	I	A	S>
195	200	205	210	215	220	225	230	235	240	*	*	*	*	*	*
TGC	TTC	TAC	TAC	GTC	GCC	ACC	ACT	TAC	TTC	CCT	CTC	CTC	CCT	CAC	CCT
ACG	AAG	ATG	ATG	CAG	CGG	TGG	TGA	ATG	AAG	GGA	GAG	GAG	GGA	GTG	GGA
C	F	Y	Y	V	A	T	T	Y	F	P	L	L	P	H	P>
245	250	255	260	265	270	275	280	285	*	*	*	*	*	*	*
CTC	TCC	TAC	TTC	GCC	TGG	CCT	CTC	TAC	TGG	GCC	TGC	CAG	GGC	TGC	GTC
GAG	AGG	ATG	AAG	CGG	ACC	GGG	GAG	ATG	ACC	CGG	ACG	GTC	CCG	ACG	CAG
L	S	Y	F	A	W	P	L	Y	W	A	C	Q	G	C	V>
290	295	300	305	310	315	320	325	330	335	*	*	*	*	*	*
CTA	ACC	GGC	GTC	TGG	GTC	ATA	GCC	CAC	AG	TGC	GGC	CAC	CAC	GCC	TTC
GAT	TGG	CCG	CAG	ACC	CAG	TAT	CGG	GTG	TTC	ACG	CCG	GTG	GTG	CGG	AAG
L	T	G	V	W	V	I	A	H	C	C	G	H	H	A	F>
340	345	350	355	360	365	370	375	380	*	*	*	*	*	*	*
AGC	GAC	TAC	CAG	TGG	CTG	GAC	GAC	ACC	GTC	GGC	CTC	ATC	TTC	CAC	TCC
TCG	CTG	ATG	GTC	ACC	GAC	CTG	CTG	TGG	CAG	CCG	GAG	TAG	AAG	GTG	AGG
S	D	Y	Q	W	L	D	D	T	V	G	L	I	F	H	S>
385	390	395	400	405	410	415	420	425	430	*	*	*	*	*	*
TTC	CTC	CTC	GTC	CCT	TAC	TTC	TCC	TGG	AAG	TAC	AGT	CAT	CGA	CGC	CAC
AAG	GAG	GAG	CAG	GGG	ATG	AAG	AGG	ACC	TTC	ATG	TCA	GTA	GCT	GCG	GTG
F	L	L	V	P	Y	F	S	W	K	Y	S	H	R	R	H>
435	440	445	450	455	460	465	470	475	480	*	*	*	*	*	*
CAT	TCC	AAC	ACT	GGC	TCC	CTC	GAG	AGA	GAC	GAA	GTG	TTT	GTC	CCC	AAG
GTA	AGG	TTG	TGA	CCG	AGG	GAG	CTC	TCT	CTG	CTT	CAC	AAA	CAG	GGG	TTC
H	S	N	T	G	S	L	E	R	D	E	V	F	V	P	K>

found in Page 2
Wild type + 129 F gen)

485	490	495	500	505	510	515	520	525
AAG	AAG	TCA	GAC	ATC	AAG	TGG	TAC	CAC
TTC	TTC	AGT	CTG	TAG	TTC	ACC	ATG	CCG
K	K	S	D	I	K	W	Y	G
530	535	540	*	545	550	*	555	560
GGA	CGC	ACC	GTG	ATG	TTA	ACG	GTT	CAG
CCT	GGG	TGG	CAC	TAC	AAT	TGC	CAA	GTC
G	R	T	V	M	L	T	V	Q
580	585	590	*	595	600	*	605	610
TAC	TTA	GCC	TTC	AAC	GTC	TCG	GGG	AGA
ATG	AAT	CGG	AAG	TTG	CAG	AGC	CCC	TCT
Y	L	A	F	N	V	S	G	R
625	630	635	*	640	645	*	650	655
TGC	CAT	TTC	CAC	CCC	AAC	GCT	CCC	ATC
ACG	GTA	AAG	GTG	GGG	TTG	CGA	GGG	TAG
C	H	F	H	P	N	A	P	I
675	680	685	*	690	695	*	700	705
CAG	ATA	TAC	ATC	TCC	GAC	GCT	GGC	ATC
GTC	TAT	ATG	TAG	AGG	CTG	CGA	CCG	TAG
Q	I	Y	I	S	D	A	G	I
725	730	735	*	740	745	*	750	755
TAC	CGC	TAC	GCT	GCT	CAA	GGA	GTT	GCC
ATG	GCG	ATG	CGA	CGA	CAG	GTT	CCT	CAA
Y	R	Y	A	A	V	Q	G	V
770	775	780	*	785	790	*	795	800
GGA	GTT	CCG	CTT	CTG	ATT	GTC	AAT	GGG
CCT	CAA	GGC	GAA	GAC	TAA	CAG	TTA	CCC
G	V	P	L	L	I	V	N	G
820	825	830	*	835	840	*	845	850
TTG	CAG	CAC	ACG	CAT	CCT	TCC	CTG	CCT
AAC	GTC	GTG	TGC	GTA	GGG	GAC	GGA	GTG
L	Q	H	T	H	P	S	L	P
865	870	875	*	880	885	*	890	895
GAT	TGG	TTG	AGG	GGA	GCT	TTG	GCC	ACC
CTA	ACC	AAC	TCC	CCT	CGA	AAC	CGG	TGG
D	W	L	R	G	A	L	A	T
915	920	925	*	930	935	*	940	945
TTG	AAC	AAG	GTC	TTC	CAC	AAT	ATC	ACG
AAC	TTG	TTC	CAG	AAG	GTG	TTA	TAG	TGC
L	N	K	V	F	H	N	I	T
965	970	975	*	980	985	*	990	995
995	1000	1005	*					

CTG TTC TCG ACC ATG CCG CAT TAT CAT GCG ATG GAA GCT ACG AAG GCG
GAC AAG AGC TGG TAC GGC GTA ATA GTA CGC TAC CTT CGA TGC TTC CGC
L F S T M P H Y H A M E A T K A>
1010 1015 1020 1025 1030 1035 1040 1045 1050 1055
* * * * * * * * * *
ATA AAG CCG ATA CTG GGA GAG TAT TAT CAG TTG CAT GGG ACG CCG GTG
TAT TTC GGC TAT GAC CCT CTC ATA ATA GTC AAC GTA CCC TGC GGC CAC
I K P I L G E Y Y Q L H G T P V>
1060 1065 1070 1075 1080 1085 1090 1095 1100
* * * * * * * * * *
GTT AAG GCG ATG TGG AGG GAG GCG AAG GAG TGT ATC TAT GTG GAA CCG
CAA TTC CGC TAC ACC TCC CTC CGC TTC CTC ACA TAG ATA CAC CTT GGC
V K A M W R E A K E C I Y V E P>
1105 1110 1115 1120 1125 1130 1135 1140 1145 1150
* * * * * * * * * *
GAC AGG CAA GGT GAG AAG AAA GGT GTG TTC TGG TAC AAC AAT AAG TTA
CTG TCC GTT CCA CTC TTC TTT CCA CAC AAG ACC ATG TTG TTA TTC AAT
D R Q G E K K G V F W Y N N K L>
1155 1160 1165 1170
* * * * *
TGA AGC AAA GAA GAA ACA AT
ACT TCG TTT CTT CTT TGT TA
* S K E E T X>

8:56 AM

5	10	15	20	25	30	35	40	45	50
*	*	*	*	*	*	*	*	*	*
ATGGGTGCAG GTGGAAGAAT GCAAGTGTCT CCTCCCTCCA AGAAGTCTGA									
TACCCACGTC CACCTTCTTA CGTTCACAGA GGAGGGAGGT TCTTCAGACT									
55	60	65	70	75	80	85	90	95	100
*	*	*	*	*	*	*	*	*	*
AACCAGACACC ATCAAGCGCG TACCCCTGCGA GACACCGCCC TTCACTGTCG									
TTGGCTGTGG TAGTTCGCGC ATGGGACGCT CTGTGGCGGG AAGTGACAGC									
105	110	115	120	125	130	135	140	145	150
*	*	*	*	*	*	*	*	*	*
GAGAACTCAA GAAAGCAATC CCACCGCACT GTTTCAAACG CTCGATCCCT									
CTCTTGAGTT CTTTCGTTAG GGTGGCGTGA CAAAGTTTGC GAGCTAGGGA									
155	160	165	170	175	180	185	190	195	200
*	*	*	*	*	*	*	*	*	*
CGCTCTTTCT CCTACCTCAT CTGGGACATC ATCATAGCCT CCTGCTTCTA									
GCGAGAAAGA GGATGGAGTA GACCCTGTAG TAGTATCGGA GGACGAAGAT									
205	210	215	220	225	230	235	240	245	250
*	*	*	*	*	*	*	*	*	*
CTACNTCGCC ACCACTTACT TCCCTCTCCT CCCTCACCCCT CTCTCCTACT									
GATGNAGCGG TGGTGAATGA AGGGAGAGGA GGGAGTGGGA GAGAGGATGA									
255	260	265	270	275	280	285	290	295	300
*	*	*	*	*	*	*	*	*	*
TCGCCCTGGCC TCTCTACTGG GCCTGCCAAG GGTGCGTCCT AACCGGGCGTC									
AGCGGACCGG AGAGATGACC CGGACGGTTC CCACGCAGGA TTGGCCGCAG									
305	310	315	320	325	330	335	340	345	350
*	*	*	*	*	*	*	*	*	*
TGGGTCATAG CCCACAGTG CGGCCACAC GCCTTCAGCG ACTACCAGTG									
ACCCAGTATC GGGTGTCAC GCGGGTGGT CGGAAGTCGC TGATGGTCAC									
355	360	365	370	375	380	385	390	395	400
*	*	*	*	*	*	*	*	*	*
GCTTGACGAC ACCGTCGGTC TCATCTTCCA CTCCCTCCTC CTCGTCCCTT									
CGAACTGCTG TGGCAGCCAG AGTAGAAGGT GAGGAAGGAG GAGCAGGGAA									
405	410	415	420	425	430	435	440	445	450
*	*	*	*	*	*	*	*	*	*
ACTTCTCCTG GAAGTACAGT CATCGCAGCC ACCATTCCAA CACTGGCTCC									
TGAAGAGGAC CTTCATGTCA GTAGCGTCGG TGGTAAGGTT GTGACCGAGG									
455	460	465	470	475	480	485	490	495	500
*	*	*	*	*	*	*	*	*	*
CTCGAGAGAG ACGAAAGTGTG TGTCCCCAAG AAGAAGTCAG ACATCAAGTG									
GAGCTCTCTC TGCTTCACAA ACAGGGGTTT TTCTTCAGTC TGTAGTTCAC									
505	510	515	520	525	530	535	540	545	550
*	*	*	*	*	*	*	*	*	*
GTACGGCAAG TACCTCAACA ACCCTTGGG ACCGACCGTG ATGTTAACGG									
CATGCCGTTC ATGGAGTTGT TGGGAAACCC TGCGTGGCAC TACAATTGCC									
555	560	565	570	575	580	585	590	595	600
*	*	*	*	*	*	*	*	*	*
TTCAGTTCAC TCTCGGCTGG CCGTTGTACT TAGCTTCAC CGTCTCGGGAA									
AAGTCAAGTG AGAGCCGACC GGCAACATGA ATCGGAAGTT GCAGAGCCCT									
605	610	615	620	625	630	635	640	645	650
*	*	*	*	*	*	*	*	*	*
AGACCTTACG ACGGCGGCTT CCGTTGCCAT TTCCACCCCA ACGCTCCCAT									

8:56 AM

Sequence Range: 1 to 1185

5	10	15	20	25	30	35	40	45							
*	*	*	*	*	*	*	*	*							
ATG	GGT	GCA	GGT	GGA	AGA	ATG	CAA	GTG	TCT	CCT	CCC	TCC	AAG	AAG	TCT
TAC	CCA	CGT	CCA	CCT	TCT	TAC	GTG	CAC	AGA	GGA	GGG	AGG	TTC	TTC	AGA
M	G	A	G	G	R	M	Q	V	S	P	P	S	K	K	S>
50	55	60	65	70	75	80	85	90	95	*	*	*	*	*	*
GAA	ACC	GAC	ACC	ATC	AAG	CGC	GTA	CCC	TGC	GAG	ACA	CCG	CCC	TTC	ACT
CTT	TGG	CTG	TGG	TAG	TTC	GCG	CAT	GGG	ACG	CTC	TGT	GGC	GGG	AAG	TGA
E	T	D	T	I	K	R	V	P	C	E	T	P	P	F	T>
100	105	110	115	120	125	130	135	140	*	*	*	*	*	*	*
GTC	GGA	GAA	CTC	AAG	AAA	GCA	ATC	CCA	CCG	CAC	TGT	TTC	AAA	CGC	TCG
CAG	CCT	CTT	GAG	TTC	TTT	CGT	TAG	GGT	GGC	GTG	ACA	AAG	TTT	GCG	AGC
V	G	E	L	K	K	A	I	P	P	H	C	F	K	R	S>
145	150	155	160	165	170	175	180	185	190	*	*	*	*	*	*
ATC	CCT	CGC	TCT	TTC	TCC	TAC	CTC	ATC	TGG	GAC	ATC	ATC	ATA	GCC	TCC
TAG	GGA	GCG	AGA	AAG	AGG	ATG	GAG	TAG	ACC	CTG	TAG	TAG	TAT	CGG	AGG
I	P	R	S	F	S	Y	L	I	W	D	I	I	I	A	S>
195	200	205	210	215	220	225	230	235	240	*	*	*	*	*	*
TGC	TTC	TAC	TAC	NTC	GCC	ACC	ACT	TAC	TTC	CCT	CTC	CTC	CCT	CAC	CCT
ACG	AAG	ATG	ATG	NAG	CGG	TGG	TGA	ATG	AAG	GGA	GAG	GAG	GGA	GTG	GGA
C	F	Y	Y	X	A	T	T	Y	F	P	L	L	P	H	P>
245	250	255	260	265	270	275	280	285	*	*	*	*	*	*	*
CTC	TCC	TAC	TTC	GCC	TGG	CCT	CTC	TAC	TGG	GCC	TGC	CAA	GGG	TGC	GTC
GAG	AGG	ATG	AAG	CGG	ACC	GGG	GAG	ATG	ACC	CGG	ACG	GTT	CCC	ACG	CAG
L	S	Y	F	A	W	P	L	Y	W	A	C	Q	G	C	V>
290	295	300	305	310	315	320	325	330	335	*	*	*	*	*	*
CTA	ACC	GGC	GTC	TGG	GTC	ATA	GCC	CAC	AAG	TGC	GGC	CAC	CAC	GCC	TTC
GAT	TGG	CCG	CAG	ACC	CAG	TAT	CGG	GTG	TTC	ACG	CCG	GTG	GTG	CGG	AAG
L	T	G	V	W	V	I	A	H	H	C	G	H	H	A	F>
340	345	350	355	360	365	370	375	380	*	*	*	*	*	*	*
AGC	GAC	TAC	CAG	TGG	CTT	GAC	GAC	ACC	GTC	GGT	CTC	ATC	TTC	CAC	TCC
TCG	CTG	ATG	GTC	ACC	GAA	CTG	CTG	TGG	CAG	CCA	GAG	TAG	AAG	GTG	AGG
S	D	Y	Q	W	L	D	D	T	V	G	L	I	F	H	S>
385	390	395	400	405	410	415	420	425	430	*	*	*	*	*	*
TTC	CTC	CTC	GTC	CCT	TAC	TTC	TCC	TGG	AAG	TAC	AGT	CAT	CGC	AGC	CAC
AAG	GAG	GAG	CAG	GGA	ATG	AAG	AGG	ACC	TTC	ATG	TCA	GTA	GCG	TCG	GTG
F	L	L	V	P	Y	F	S	W	K	Y	S	H	R	S	H>
435	440	445	450	455	460	465	470	475	480	*	*	*	*	*	*
CAT	TCC	AAC	ACT	GGC	TCC	CTC	GAG	AGA	GAC	GAA	GTG	TTT	GTC	CCC	AAG
GTA	AGG	TTC	TGA	CCG	AGG	GAG	CTC	TCT	CTG	CTT	CAC	AAA	CAG	GGG	TTC
H	S	N	T	G	S	L	E	R	D	E	V	F	V	P	K>

485	490	495	500	505	510	515	520	525							
*	*	*	*	*	*	*	*	*							
AAG	AAG	TCA	GAC	ATC	AAG	TGG	TAC	GGC	AAG	TAC	CTC	AAC	AAC	CCT	TTG
TTC	TTC	AGT	CTG	TAG	TTC	ACC	ATG	CCG	TTC	ATG	GAG	TTG	TTG	GGA	AAC
K	K	S	D	I	K	W	Y	G	K	Y	L	N	N	P	L>
530	535	540	545	550	555	560	565	570	575	*	*	*	*	*	*
GGA	CGC	ACC	GTG	ATG	TTA	ACG	GTT	CAG	TTC	ACT	CTC	GGC	TGG	CCG	TTG
CCT	GCG	TGG	CAC	TAC	AAT	TGC	CAA	GTC	AAG	TGA	GAG	CCG	ACC	GGC	AAC
G	R	T	V	M	L	T	V	Q	F	T	L	G	W	P	L>
580	585	590	595	600	605	610	615	620	*	*	*	*	*	*	*
TAC	TTA	GCC	TTC	AAC	GTC	TCG	GGG	AGA	CCT	TAC	GAC	GGC	GGC	TTC	CGT
ATG	AAT	CGG	AAG	TTG	CAG	AGC	CCT	TCT	GGG	ATG	CTG	CCG	CCG	AAG	GCA
Y	L	A	F	N	V	S	G	R	P	Y	D	G	G	F	R>
625	630	635	640	645	650	655	660	665	670	*	*	*	*	*	*
TGC	CAT	TTC	CAC	CCC	AAC	GCT	CCC	ATC	TAC	AAC	GAC	CGC	GAG	CGT	CTC
ACG	GTA	AAG	GTG	GGG	TTG	CGA	GGG	TAG	ATG	TTG	CTG	GCG	CTC	GCA	GAG
C	H	F	H	P	N	A	P	I	Y	N	D	R	E	R	L>
675	680	685	690	695	700	705	710	715	720	*	*	*	*	*	*
CAG	ATA	TAC	ATC	TCC	GAC	GCT	GGC	ATC	CTC	GCC	GTC	TGC	TAC	GGT	CTC
GTC	TAT	ATG	TAG	AGG	CTG	CGA	CCG	TAG	GAG	GGG	CAG	ACG	ATG	CCA	GAG
Q	I	Y	I	S	D	A	G	I	L	A	V	C	Y	G	L>
725	730	735	740	745	750	755	760	765	*	*	*	*	*	*	*
TTC	CGT	TAC	GCC	GCC	GGC	CAG	GGG	GTG	GCC	TCG	ATG	GTC	TGC	TTC	TAC
AAG	GCA	ATG	CGG	CGG	CCG	GTC	CCT	CAC	CGG	AGC	TAC	CAG	ACG	AAG	ATG
F	R	Y	A	A	G	Q	G	V	A	S	M	V	C	F	Y>
770	775	780	785	790	795	800	805	810	815	*	*	*	*	*	*
GGA	GTC	CCG	CTT	CTG	ATT	GTC	AAT	GGT	TTC	CTC	GTG	TTG	ATC	ACT	TAC
CCT	CAG	GGC	GAA	GAC	TAA	CAG	TTA	CCA	AAG	GAG	CAC	AAC	TAG	TGA	ATG
G	V	P	L	L	I	V	N	G	F	L	V	L	I	T	Y>
820	825	830	835	840	845	850	855	860	*	*	*	*	*	*	*
TTG	CAG	CAC	ACG	CAT	CCT	TCC	CTG	CCT	CAC	TAC	GAT	TCG	TCC	GAG	TGG
AAC	GTC	GTG	TGC	GTA	GGG	GAC	GGG	GTG	ATG	CTA	AGC	AGG	CTC	ACC	
L	Q	H	T	H	P	S	L	P	H	Y	D	S	S	E	W>
865	870	875	880	885	890	895	900	905	910	*	*	*	*	*	*
GAT	TGG	TTC	AGG	GGA	GCT	TTG	GCT	ACC	GTT	GAC	AGA	GAC	TAC	GGA	ATC
CTA	ACC	AAG	TCC	CCT	CGA	AAC	CGA	TGG	CAA	CTG	TCT	CTG	ATG	CCT	TAG
D	W	F	R	G	A	L	A	T	V	D	R	D	Y	G	I>
915	920	925	930	935	940	945	950	955	960	*	*	*	*	*	*
TTG	AAC	AAG	GTC	TTC	CAC	AAT	ATT	ACC	GAC	ACG	CAC	GTG	GCC	CAT	CAT
AAC	TTG	TTC	CAG	AAG	GTG	TTA	TAA	TGG	CTG	TGC	GTG	CAC	CGG	GTA	GTA
L	N	K	V	F	H	N	I	T	D	T	H	V	A	H	H>
965	970	975	980	985	990	995	1000	1005	*	*	*	*	*	*	*

CCG TTC TCC ACG ATG CCG CAT TAT CAC GCG ATG GAA GCT ACC AAG GCG
GGC AAG AGG TGC TAC GGC GTA ATA GTG CGC TAC CTT CGA TGG TTC CGC
P F S T M P H Y H A M E A T K A>
1010 1015 1020 1025 1030 1035 1040 1045 1050 1055
* * * * * * * * * *
ATA AAG CCG ATA CTG GGA GAG TAT TAT CAG TTC GAT GGG ACG CCG GTG
TAT TTC GGC TAT GAC CCT CTC ATA ATA GTC AAG CTA CCC TGC GGC CAC
I K P I L G E Y Y Q F D G T P V>
1060 1065 1070 1075 1080 1085 1090 1095 1100
* * * * * * * * * *
GTT AAG GCG ATG TGG AGG GAG GCG AAG GAG TGT ATC TAT GTG GAA CCG
CAA TTC CGC TAC ACC TCC CTC CGC TTC CTC ACA TAG ATA CAC CTT GGC
V K A M W R E A K E C I Y V E P>
1105 1110 1115 1120 1125 1130 1135 1140 1145 1150
* * * * * * * * * *
GAC AGG CAA GGT GAG AAG AAA GGT GTG TTC TGG TAC AAC AAT AAG TTA
CTG TCC GTT CCA CTC TTC TTT CCA CAC AAG ACC ATG TTG TTA TTC AAT
D R Q G E K K G V F W Y N N K L>
1155 1160 1165 1170 1175 1180 1185
* * * * * * * * * *
TGA GGA TAT GAT GAT GGT GAA AGA AAT CAC TAG
ACT CCT ATA CTA CTA CCA CTT TCT TTA GTG ATC
* G Y D D G E R N H *>